Page 2, line 2, delete "Triticum aestivum" and substitute --*Triticum aestivum* --.

Page 2, line 5, delete "by claims 1 to 10", and substitute --as follows--.

Pages 4-12, delete the pages in their entirety, and substitute the pages set forth as Attachment "A".

Page 14, line 11, delete "even".

Page 15, lines 10-11, delete "for about minutes".

IN THE CLAIMS

1. (amended) A set of microsatellite markers [(based on hypervariable genome sections)] for plants of the *Triticum aestivum* species [, as well as of] and the [Tribe] tribe Triticeae [using the polymerase chain reaction (PCR), wherein] , each of said markers comprising a sequence tagged site (STS) , which is defined by [two specific] a pair of primers, specific to a particular microsatellite sequence, each primer having an [which] average [a] length of 20 ± 3 bases and [flank] flanking the

particular [a] microsatellite sequence, wherein each of said [which] microsatellite markers [are amplified to polymorphisms (PCR products of] is formed by amplification of the microsatellite sequence by a polymerase chain reaction, to form markers of different length [)], wherein the primer pairs are selected from at least one of the pairs SEQ ID NO. x and SEQ ID NO. $x + 1$, where x = odd numbers from 1 through 465.

2. (twice amended) The [microsatellite markers] set of claim 1, wherein the microsatellite sequence is a tandem-repetitive n-fold repetition of a di-, tri-, or tetranucleotide sequence, in which $n \geq 10$.

3. (twice amended) The [microsatellite markers] set of claim 1, wherein the microsatellite sequence is a composite microsatellite sequence.

4. (twice amended) The [microsatellite markers] set of claim 1, wherein the microsatellite sequence is an imperfect sequence, in which individual bases are mutated.

Cancel claim 5.

6. (twice amended) A [method for the preparation of a microsatellite marker [of claim 1 for plants of the

Triticum aestivum] for species [as well] of the [Tribe] tribe Triticeae, [wherein] comprising the steps of:

amplifying a microsatellite sequence, in the presence of two specific primers flanking the sequence, with a [hypervariable genome sections (so-called microsatellites), with the help of the] polymerase chain reaction [(PCR), are amplified],

separating the amplified microsatellite sequence [subsequently separated] and [detected]

identifying the separated sequence as a particular [to polymorphous] polymorphic fragment [fragments in the presence of two specific primers which flank a microsatellite sequence to the left and right of each microsatellite locus], the two primers being chosen as SEQ ID NO. x and SEQ ID NO. $x + 1$, where x = odd numbers from 1 through 465.

7. (twice amended) The method of claim 6, wherein a gel chosen from the group consisting of highly resolving agarose gels, native polyacrylamide gels [or] and denaturing polyacrylamide gels are used for the [separation of the markers] separating step.